



REPLACEMENT SHEETS
 Express Mail No.: EV767822197US Deposited: 03/08/2007
 Title: TARGETED GLYCOSAMINOGLYCAN POLYMERS BY POLYMER
 GRAFTING AND METHODS OF MAKING AND USING SAME
 Inventors: Paul L. DeAngelis et al. Group: 1656
 Filed: Herewith Examiner: N. Nashed
 Agent: Kathryn L. Hester Dkt. No.: 35542.097
 SHEET 18 OF 41 Formal Drawings

Figure 15C

Multalin version 5.4.1
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 Published research using this software should cite.
 Multiple sequence alignment with hierarchical clustering
 F. CORPET, 1988, Nucl. Acids Res., 16 (22), 10881-10890

Symbol comparison table: blosum62

Gap weight: 12

Gap length weight: 2

Consensus levels: high=90% low=50%

Consensus symbols:

! is anyone of IV

\$ is anyone of LM

* is anyone of FY

is anyone of NDQEBZ

MSF:	651	Check:	0	..	
Name: A	Len:	651	Check:	612	Weight: 0.58
Name: B	Len:	651	Check:	249	Weight: 0.58
Name: pglA	Len:	651	Check:	7677	Weight: 1.08
Name: DcbF	Len:	651	Check:	7537	Weight: 1.76
Name: Consensus	Len:	651	Check:	5816	Weight: 0.00

//

	1	50
A2	MSLFKR ATELFKSGNY KDALTLYENI
B10	MSLFKR ATELFKSGNY KDALTLYENI
pglA	MKRKKEMTQK QMTKNPPQHE KENEINTFQN KIDSLLKTTLN KDIISQQTLL	
DcbF	MSLFKR ATELFKSGNY KDALTLYENI
sensus	\$s1Fkr at#lfKsgny KDaltlyeni
	51	100
A2	AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENKF....	
B10	AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENKF....	
pglA	AKQDSKHPLS ASLENENKLL LKOLOLVILOE FEKIYTQNA LEAKLEKDKQ	
DcbF	AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENEF....	
Consensus	AKiyg....S eSlvkyNidi cKk.#itqsk s#KleedNis gEnkf....	
	101	150
A2	SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSNTEK FIEASINSL	
B10	SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSNTEK FIEASINSL	
pglA	TTSITDLYNE VAKSDLGLVK ETNSVNPLVS IIMTSNNTAQ FIEASINSL	
DcbF	SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSNTEK FIEASINSL	
Consensus	svSIkDLYNE !snS#LGItK ErlgappPLVS IIMTSNNTek FIEASINSL	
	151	200
A2	LQTYNNELEVI VVDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTYFAKN	
B10	LQTYNNELEVI VVDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTYFAKN	
pglA	LQTYNNELEVI VVDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTYFAKN	
DcbF	LQTYNNELEVI VVDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTYFAKN	
Consensus	LQTYNNELEVI VVDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTYFAKN	

Fig. 15C cont'd

201	250
A2	TGILKSKGDI IFFQDSDDVC HHERIERCVN ALLSNKDNIA VRCAYSRINL
B10	TGILKSKGDI IFFQDSDDVC HHERIERCVN ALLSNKDNIA VRCAYSRINL
pg1A	TGILKSKGDI IFFQDSDDVC HHERIERCVN ILLANKETIA VRCAYSRLAP
DcbF	TGILKSKGDI IFFQDSDDVC HHERIERCVN ALLSNKDNIA VRCAYSRINL
Consensus	TGILKSKGDI IFFQDSDDVC HHERIERCVN aLLsNK#nIA VRCAYSRinL
251	300
A2	ETQNIIKVND NKYKLGTLT GVYRKVFNEI GFFNCTTKAS DDEFYHRIIK
B10	ETQNIIKVND NKYKLGTLT GVYRKVFNEI GFFNCTTKAS DDEFYHRIIK
pg1A	ETQHIIKVNN MDYRLGFITL GMHRKVFOEI GFFNCTTKGS DDEFFHRIAK
DcbF	ETQNIIKVND NKYKLGTLT GVYRKVFNEI GFFNCTTKAS DDEFYHRIIK
Consensus	ETQnIiKVN# nkYkLGTLT GvYRKVF#EI GFFNCTTKaS DDEF%HRIIK
301	350
A2	YYGKNRINNL FLPLYYNTMR EDLSLFSDMVE WVDENNIKQK TSDARQNYLH
B10	YYGKNRINNL FLPLYYNTMR EDLSLFSDMVE WVDENNIKQK TSDARQNYLH
pg1A	YYGKEKIKNL LLPLYYNTMR ENSLFTDMVE WIDNHNIIQK MSDTROHYAT
DcbF	YYGKNRINNL FLPLYYNTMR EDLSLFSDMVE WVDENNIKQK TSDARQNYLH
Consensus	YYGK#rInNL flPLYYNTMR E#SLFsdMVE W!D#nNIkQK tSDaRQnYlh
351	400
A2	EFQKIHNERK LNELKEIFSf PRIHDALPIS KEMSKLSNPk IPVYINICSI
B10	EFQKIHNERK LNELKEIFSf PRIHDALPIS KEMSKLSNPk IPVYINICSI
pg1A	LFQAMHNETA SHDFKNLFQF PRIYDALPVP OEMSKLSNPk IPVYINICSI
DcbF	EFQKIHNERK FNELKEIFSf PRIHDALPIS KEMSKLSNPk IPVYINICSI
Consensus	eFQkiHNERk .n#1K#iFsF PRIhDALP!s KEMSKLSNPk IPVYINICSI
401	450
A2	PSRIKQLQYT IGVLKNQCDH FHIYLDGYPE VPDFIKKLGn KATVINCQNK
B10	PSRIKQLQYT IGVLKNQCDH FHIYLDGYPE VPDFIKKLGn KATVINCQNK
pg1A	PSRIAQLRRI IGILKNQCDH FHIYLDGYVE IPDFIKNLGN KATVvHCKDK
DcbF	PSRIKQLQYT IGVLKNQCDH FHIYLDGYPE VPDFIKKLGn KATVINCQNK
Consensus	PSRIKQLqyt IG!LKNQCDH FHIYLDGYpE !PDFIKkLGn KATV!nCq#K
451	500
A2	NESIRDNGKF ILLEKLIKEN KDGYYITCDD DIRYPADYTN TMIKKINKYN
B10	NESIRDNGKF ILLEKLIKEN KDGYYITCDD DIRYPADYIN TMIKKINKYN
pg1A	DNSIRDNGKF ILLEELIEKN QDGYYITCDD DIIYPSDYIN TMIKKLNNEYD
DcbF	NESIRDNGKF ILLEKLIKEN KDGYYITCDD DIRYPADYIN TMIKKINKYN
Consensus	##SIRDNGKF ILLEkLIken KDGYYITCDD DIRYPaDYin TMIKKINKY#
501	550
A2	DKAAIGLHGv IFPSRVNKF SSDRIVYNFQ KPLENDTAVN ILGTGTVAFR
B10	DKAAIGLHGv IFPSRVNKF SSDRIVYNFQ KPLENDTAVN ILGTGTVAFR
pg1A	DKAVIGLHGv IIFPSRMTKF SADRLVYSFY KPLEKDKAVN VLGTGTVSFR
DcbF	DKAAIGLHGv IFPSRVNKF SSDRIVYNFQ KTFRK.....
Consensus	DKAaIGLHG! IFPSRvnKF SsDRiVYnFq Kplekd.avn .lgtgtv.fr
551	600
A2	VSIFNKFSLs DFEHPGMVDI YFSILCKNN ILQVCISRPS NWLTEDNKNT
B10	VSIFNKFSLs DFEHPGMVDI YFSILCKNN ILQVCISRPS NWLTEDNKNT
pg1A	VSLFNQFSLS DFTHSGMADI YFSLLCKNN ILQICISRPA NWLTEDNRDS
DcbF
Consensus	vs.fn.fsls df.h.gm.di yfs.lcknn ilq.cisrp. nwltedn...

Fig. 15C cont'd

	601		650		
A2	ETLFHEFQNR	DEIQSKLIIS	NNPWGYSSIIY	PLNNNNANYS	ELIPCLSFYN
B10	ETLFHEFQNR	DEIQSKLIIS	NNPWGYSSIIY	PLNNNNANYS	ELIPCLSFYN
pg1A	ETLYHQYRDN	DEQQTQLIME	NGPWGYSSIIY	PLVKNHPKFT	DLIPCLPFYF
DcbF
Consensus	etl.h.....	de.q..li..	n.pwgyssiy	pl..n.....	.lipcl.fy.
	651				
A2	E				
B10	E				
pg1A	L				
DcbF	.				
Consensus	.				

Figure 15D

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 Multiple sequence alignment with hierarchical clustering
 F. CORPET, 1988, Nucl. Acids Res., 16 (22), 10881-10890
 Symbol comparison table: blosum62
 Gap weight: 12
 Gap length weight: 2
 Consensus levels: high=90% low=50%
 Consensus symbols:
 ! is anyone of IV
 \$ is anyone of LM
 % is anyone of FY
 # is anyone of NDQEBZ

MSF:	651	Check:	0	
Name:	pmHS	Len:	651	Check: 612 Weight: 0.75
Name:	pglA	Len:	651	Check: 7677 Weight: 0.75
Name:	DcbF	Len:	651	Check: 7537 Weight: 1.49
Name:	Consensus	Len:	651	Check: 5816 Weight: 0.00

//

	1	50
pmHS	MSLFKR ATELFKSGNY KDALTLYENI
pglA	MKRKKEMTQK QMTKNPPQHE KENELNTFQN KIDSLKTTLN KDIISQOTLL	
DcbF	MSLFKR ATELFKSGNY KDALTLYENI
Consensus	\$slFkr at#lfKsgny KDaltlyeni
	51	100
pmHS	AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENKF.	
pglA	AKQDSKHPLS ASLENENKLL LKQLQLVLQE FEKIYTYNQA LEAKLEKDKQ	
DcbF	AKIYG....S ESLVKYNIDI CKK.NITQSK SNKIEEDNIS GENEF.	
Consensus	AKiyg....S eSlvkyNidi cKk.#itqsk s#KieedNis gEnkf.	
	101	150
pmHS	SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSHNTEK FIEASINSLL	
pglA	TTSITDLYNE VAKSDLGLVK ETNSVNPLVS IIMTSHNTAQ FIEASINSLL	
DcbF	SVSIKDLYNE ISNSELGITK ERLGAPPLVS IIMTSHNTEK FIEASINSLL	
Consensus	svSIKDLYNE !snS#LGitK ErlgapPLVS IIMTSHNTek FIEASINSLL	
	151	200
pmHS	LQTYNNELEVI VVDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTYFAKN	
pglA	LQTYKNIEII IVDDDSSDNT FEIASRIANT TSKVRVFRNL SNLGTYFAKN	
DcbF	LQTYNNELEVI VVDDYSTDKT FQIASRIANS TSKVKTFRNL SNLGTYFAKN	
Consensus	LQTynNLE!I !VDDyStDkt F#IASRIANS TSKVktFRNL SNLGTYFAKN	
	201	250
pmHS	TGILKSKGDI IFFQDSDDVC HHERIERCVN ALLSNKDNIA VRCAYSRINL	
pglA	TGILKSKGDI IFFQDSDDVC HHERIERCVN ILLANKETIA VRCAYSRLAP	
DcbF	TGILKSKGDI IFFQDSDDVC HHERIERCVN ALLSNKDNIA VRCAYSRINL	
Consensus	TGILKSKGDI IFFQDSDDVC HHERIERCVN aLLsNK#nIA VRCAYSRinl	
	251	300
pmHS	ETQNIIKVND NKYKLGLITL GVYRKVFNEI GFFNCTTKAS DDEFYHRIIK	
pglA	ETQHIIKVNN MDYRLGFITL GMHRKVFQEI GFFNCTTKGS DDEFFHRIAK	
DcbF	ETQNIIKVND NKYKLGLITL GVYRKVFNEI GFFNCTTKAS DDEFYHRIIK	
Consensus	ETQnIIKV# nkYkLGLITL GvyRKVF#EI GFFNCTTKaS DDEF%HRIik	

Figure 15D cont'd

	301	350			
pmHS	YYGKNRINNL	FLPLYYNTMR	EDSLFSDMVE	WVDENNIKQK	TSDARQNYLH
pg1A	YYGKEKIKNL	LLPLYYNTMR	ENSLFTDMVE	WIDNHNIIQK	MSDTRQHYAT
DcbF	YYGKNRINNL	FLPLYYNTMR	EDSLFSDMVE	WVDENNIKQK	TSDARQNYLH
Consensus	YYGK#rInNL	FLPLYYNTMR	E#SLFsDMVE	W:D#nNIkQK	tSDaRQnYlh
	351	400			
pmHS	EFOKIHNERK	LNELKEIFSF	PRIHDALPIS	KEMSKLSNPK	IPVYINICSI
pg1A	LFQAMHNETA	SHDFKNLFQF	PRIYDALPVP	QEMSKLSNPK	IPVYINICSI
DcbF	EFOKIHNERK	FNELKEIFSF	PRIHDALPIS	KEMSKLSNPK	IPVYINICSI
Consensus	eFQkiHNERk	.n#lK#iFsF	PRIhDALP!s	KEMSKLSNPK	IPVYINICSI
	401	450			
pmHS	PSRIKQLQYT	IGVLKNQCDH	FHIYLDGYPE	VPDFIKKLGN	KATVINCQNK
pg1A	PSRIAQLRRI	IGILKNQCDH	FHIYLDGYVE	IPDFIKNLGN	KATVVHCKDK
DcbF	PSRIKQLQYT	IGVLKNQCDH	FHIYLDGYPE	VPDFIKKLGN	KATVINCQNK
Consensus	PSRIKQLqyt	IG!LKNQCDH	FHIYLDGYpE	!PDFIKKLGN	KATV!nCq#K
	451	500			
pmHS	NESIRDNGKF	ILLEKLIKEN	KDGYYITCDD	DIRYPADYTN	TMIKKINKYN
pg1A	DNSIRDNGKF	ILLEELIEKN	QDGYYITCDD	DIYPSDYIN	TMIKKLNEYD
DcbF	NESIRDNGKF	ILLEKLIKEN	KDGYYITCDD	DIRYPADYIN	TMIKKINKYN
Consensus	##SIRDNGKF	ILLEkLIkeN	kDGYYITCDD	DirYPaDYin	TMIKKINKY#
	501	550			
pmHS	DKAAIGLHG	IFPSRVNKYF	SSDRIVYNFQ	KPLENDTAVN	ILGTGTVAFR
pg1A	DKAVIGLHG	IFPSRMTKYF	SADRIVYSFY	KPLEDKAVN	VLGTGTVSFR
DcbF	DKAAIGLHG	IFPSRVNKYF	SSDRIVYNFQ	KTFRK.....
Consensus	DKAaIGLHG!	ifPSRvnKYF	SsDRiVYnFq	Kplekd.avn	.lgtgtv.fr
	551	600			
pmHS	VSIFNKFSL	DFEHPGMVDI	YFSILCKKNN	ILQVCISRPS	NWLTEDNKNT
pg1A	VSLFNQFSL	DFTHSGMADI	YFSLLCKKNN	ILQICISRPA	NWLTEDNRDS
DcbF
Consensus	vs.fn.fs1s	df.h.gm.di	yfs.lckknn	ilq.cisrp.	nwltedn...
	601	650			
pmHS	ETLFHEFQNR	DEIQSKLIIS	NNPwgYssiY	PLLNNNNANYS	ELIPCLSFY
pg1A	ETLYHQYRDN	DEQQTQLIME	NGPwgYssiY	PLVKNHPKFT	DLIPCLPFY
DcbF
Consensus	etl.h.....	de.q..li..	n.pwgYssiY	pl..n.....	.lipcl.fy.
	651				
pmHS	E				
pg1A	L				
DcbF	.				
Consensus	.				